US 90
0320

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/896,692_
Source: _OIPE_
Date Processed by STIC: _3/18/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
    http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or** ther delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/896,692_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
     Wrapped Aminos _

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
     Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
     "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
     (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
     (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
     (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10_____Invalid <213>
     Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)

12_____PatentIn 2.0
     "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 03/18/2002
PATENT APPLICATION: US/09/896,692   TIME: 14:56:37

Input Set : **A:\47508-556 (HYZ-069).ST25.txt**
Output Set: **N:\CRF3\03182002\I896692.raw**

Does Not Comply
Corrected Diskette Needed

```
 4 <110> APPLICANT: Agrawal, Sudhir
 6 <120> TITLE OF INVENTION: Novel HIV-Specific Synthetic Oligonucleotides and Methods of
Their Use
 8 <130> FILE REFERENCE: 47508.556 (HYZ-069)
10 <140> CURRENT APPLICATION NUMBER: US 09/896,692
11 <141> CURRENT FILING DATE: 2001-06-29
13 <150> PRIOR APPLICATION NUMBER: US 08/914,827
14 <151> PRIOR FILING DATE: 1997-08-19
16 <160> NUMBER OF SEQ ID NOS: 8
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

ERRORED SEQUENCES

```
      20 <210> SEQ ID NO: 1
      21 <211> LENGTH: 21
      22 <212> TYPE: RNA
      23 <213> ORGANISM: Artificial Sequence
      25 <220> FEATURE:
      26 <223> OTHER INFORMATION: oligonucleotide
      28 <400> SEQUENCE: 1
E--> 29 ucgcacccat ctctctccuu c
      42 <210> SEQ ID NO: 3
      43 <211> LENGTH: 21
      44 <212> TYPE: RNA
      45 <213> ORGANISM: Artificial Sequence
      47 <220> FEATURE:
      48 <223> OTHER INFORMATION: oligonucleotide
      50 <400> SEQUENCE: 3
E--> 51 cgcacccatc tctctccuuc u
      75 <210> SEQ ID NO: 6
      76 <211> LENGTH: 21
      77 <212> TYPE: RNA
      78 <213> ORGANISM: Artificial Sequence
      80 <220> FEATURE:
      81 <223> OTHER INFORMATION: oligonucleotide
      83 <400> SEQUENCE: 6
E--> 84 tcgcacccat ctctctcctt c
      94 <210> SEQ ID NO: 8
      95 <211> LENGTH: 41
      96 <212> TYPE: DNA
      97 <213> ORGANISM: Artificial Sequence
      99 <220> FEATURE:
     100 <223> OTHER INFORMATION: oligonucleotide
```

insufficient explanation - give source of genetic material

t's not allowed in an RNA sequence

21 *(see item 11 on Error Summary Sheet)*

21 *same error as above*

21 *same error*

see p.2

Please correct this error globally.

RAW SEQUENCE LISTING   DATE: 03/18/2002
PATENT APPLICATION: US/09/896,692   TIME: 14:56:37

Input Set : A:\47508-556 (HYZ-069).ST25.txt
Output Set: N:\CRF3\03182002\I896692.raw

```
      102 <400> SEQUENCE: 8
      103 cggaggctag aaggagagag atgggtgcga gagcgtcagt a          41
E-->  104 47508-556(hyZ-069).st25
E-->  106 Page 1
```

delete

VERIFICATION SUMMARY   DATE: 03/18/2002
PATENT APPLICATION: US/09/896,692   TIME: 14:56:38

Input Set : **A:\47508-556 (HYZ-069).ST25.txt**
Output Set: **N:\CRF3\03182002\I896692.raw**

L:29 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:4
L:51 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:4
L:84 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:7
L:104 M:254 E: No. of Bases conflict, LENGTH:Input:25 Counted:51 SEQ:8
L:104 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17
L:104 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=8
L:106 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:106 M:252 E: No. of Seq. differs, <211>LENGTH:Input:41 Found:55 SEQ:8